Supplemental Table I – 'Light' and 'heavy' MRM fragmentation transitions are provided along with the optimized fragmentation parameters for all targeted peptides as grouped together for each protein of interest, and within each fused polypeptide. Precursor and product ion transitions listed in black were used for quantification; those transitions listed in red were used for quantitative validation only.

Supplemental Table II – Proteins were normalized to strep tag concentration ratios and to DLG4 (PSD-95). Normalization factors to strep tag are provided for each fused polypeptide (clones), and normalization to DLG4 is provided for each sample preparation.

Supplemental Table III – The origin of quantitative variability is demonstrated based on the measurement mean for peptide ion abundance ratios averaged among all samples. Mean, *SD*, and % CV values are provided for 'within transition', 'within peptide', and 'within protein' calculations (i.e. sample preparation variability, variability among ions from the same peptide, and variability among peptides from the same protein, respectively).

Supplemental Figure I: Primary amino acid sequence of the fused polypeptides from expression of each of eight QconCAT clone constructs. The peptide sequences targeted by MRM are provided below, along with the name of each native protein precursor and the amino acid position of the N- and C-terminal amino acids found in the native protein. Tryptic cleavage sites (K and R) are highlighted in yellow. Flanking sequences are bordered by red (|) vertical lines. The strep tag sequence is shown in bold at the C-terminus of each fused polypeptide.